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112745
OIEP.

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/784,674

DATE: 11/23/2001
 TIME: 15:54:54

Input Set : N:\Crf3\RULE60\09784674.txt
 Output Set: C:\CRF31113\REFHOLD\I784674.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Shannon, Karen W.

7 Wolber, Paul K.

8 Delenstarr, Glenda C.

9 Webb, Peter G.

10 Kincaid, Robert H.

12 (ii) TITLE OF INVENTION: Methods for evaluating oligonucleotide
13 probe sequences

15 (iii) NUMBER OF SEQUENCES: 1165

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
19 Company M/S 20BO

20 (B) STREET: 3000 Hanover Street

21 (C) CITY: Palo Alto

22 (D) STATE: CA

23 (E) COUNTRY: USA

24 (F) ZIP: 94304

26 (v) COMPUTER READABLE FORM:

27 (A) MEDIUM TYPE: Floppy disk

28 (B) COMPUTER: IBM PC compatible

29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

32 (vi) CURRENT APPLICATION DATA:

C--> 33 (A) APPLICATION NUMBER: US/09/784,674

C--> 34 (B) FILING DATE: 15-Feb-2001

35 (C) CLASSIFICATION: Not available

38 (vii) PRIOR APPLICATION DATA:

39 (A) APPLICATION NUMBER: 09/021,701

40 (B) FILING DATE: 10-FEB-1998

43 (viii) ATTORNEY/AGENT INFORMATION:

44 (A) NAME: Choi, Wendy A.

45 (B) REGISTRATION NUMBER: 36,697

46 (C) REFERENCE/DOCKET NUMBER: 10971464-1

48 (ix) TELECOMMUNICATION INFORMATION:

49 (A) TELEPHONE: 650-236-2386

50 (B) TELEFAX: 650-852-8063

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 24 base pairs

57 (B) TYPE: nucleic acid

58 (C) STRANDEDNESS: single

59 (D) TOPOLOGY: linear

61 (ii) MOLECULE TYPE: cDNA

63 (iii) HYPOTHETICAL: YES

65 (iv) ANTI-SENSE: NO

68 (ix) FEATURE:

ENTERED

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```

69      (A) NAME/KEY: stem_loop
70      (B) LOCATION: 2..21
73      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
75 ACTGGCAATC ACAATTGCCA GTAA
77 (2) INFORMATION FOR SEQ ID NO: 2:
79      (i) SEQUENCE CHARACTERISTICS:
80          (A) LENGTH: 75 base pairs
81          (B) TYPE: nucleic acid
82          (C) STRANDEDNESS: single
83          (D) TOPOLOGY: linear
85      (ii) MOLECULE TYPE: tRNA
87      (iii) HYPOTHETICAL: NO
89      (iv) ANTI-SENSE: NO
91      (vi) ORIGINAL SOURCE:
92          (A) ORGANISM: Saccharomyces cerevisiae
94      (ix) FEATURE:
95          (A) NAME/KEY: tRNA
96          (B) LOCATION: 1..75
97          (C) IDENTIFICATION METHOD: experimental
98          (D) OTHER INFORMATION: /function= "transfer RNA"
99 /product= "tRNA-Ala"
100 /evidence= EXPERIMENTAL
101 /anticodon= (pos: 34 .. 36, aa: Ala)
102 /citation= ([1][2])
104      (ix) FEATURE:
105          (A) NAME/KEY: modified_base
106          (B) LOCATION: 9
107          (C) IDENTIFICATION METHOD: experimental
108          (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
109 /frequency= 0.9999
110 /mod_base= mlg
111 /citation= ([1][2])
113      (ix) FEATURE:
114          (A) NAME/KEY: modified_base
115          (B) LOCATION: 16
116          (C) IDENTIFICATION METHOD: experimental
117          (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
118 /frequency= 0.9999
119 /mod_base= d
120 /citation= ([1][2])
122      (ix) FEATURE:
123          (A) NAME/KEY: modified_base
124          (B) LOCATION: 20
125          (C) IDENTIFICATION METHOD: experimental
126          (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
127 /frequency= 0.9999
128 /mod_base= d
129 /citation= ([1][2])
131      (ix) FEATURE:

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132      (A) NAME/KEY: modified_base
133      (B) LOCATION: 26
134      (C) IDENTIFICATION METHOD: experimental
135      (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
136 /frequency= 0.9999
137 /mod_base= m22g
138 /citation= ([1][2])
140      (ix) FEATURE:
141      (A) NAME/KEY: modified_base
142      (B) LOCATION: 34
143      (C) IDENTIFICATION METHOD: experimental
144      (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
145 /frequency= 0.9999
146 /mod_base= i
147 /citation= ([1][2])
149      (ix) FEATURE:
150      (A) NAME/KEY: modified_base
151      (B) LOCATION: 37
152      (C) IDENTIFICATION METHOD: experimental
153      (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
154 /frequency= 0.9999
155 /mod_base= mli
156 /citation= ([1][2])
158      (ix) FEATURE:
159      (A) NAME/KEY: modified_base
160      (B) LOCATION: 38
161      (C) IDENTIFICATION METHOD: experimental
162      (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
163 /frequency= 0.9999
164 /mod_base= p
165 /citation= ([1][2])
167      (ix) FEATURE:
168      (A) NAME/KEY: modified_base
169      (B) LOCATION: 46
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171      (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
172 /frequency= 0.9999
173 /mod_base= d
174 /citation= ([1][2])
176      (ix) FEATURE:
177      (A) NAME/KEY: modified_base
178      (B) LOCATION: 53
179      (C) IDENTIFICATION METHOD: experimental
180      (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
181 /frequency= 0.9999
182 /mod_base= t
183 /citation= ([1][2])
185      (ix) FEATURE:
186      (A) NAME/KEY: modified_base
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187          (B) LOCATION: 54
188          (C) IDENTIFICATION METHOD: experimental
189          (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
190 /frequency= 0.9999
191 /mod_base= p
192 /citation= ([1][2])
194      (x) PUBLICATION INFORMATION:
195          (A) AUTHORS: Holley, R. W.
196 Apgar, J.
197 Everett, G. A.
198 Madison, J. T.
199 Marquisee, M.
200 Merrill, S. H.
201 Penswick, J. R.
202 Zamir, A.
203          (B) TITLE: Structure of a ribonucleic acid
204          (C) JOURNAL: Science
205          (D) VOLUME: 147
206          (F) PAGES: 1462-1465
207          (G) DATE: 1965
208          (K) RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 75
210      (x) PUBLICATION INFORMATION:
211          (A) AUTHORS: Penswick, J. R.
212 Martin, R.
213 Dirheimer, G.
214          (B) TITLE: Evidence supporting a revised sequence for
215 yeast alanine tRNA
216          (C) JOURNAL: FEBS Lett.
217          (D) VOLUME: 50
218          (F) PAGES: 28-31
219          (G) DATE: 1975
220          (K) RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 75
223      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
225 GGGCGUGUGG CGUAGUCGGU AGCGCGCUCC CUUGGCGUGG GAGAGUCUCC GGUUCGAUUC      60
227 CGGACUCGUC CACCA      75
229 (2) INFORMATION FOR SEQ ID NO: 3:
231      (i) SEQUENCE CHARACTERISTICS:
232          (A) LENGTH: 16 base pairs
233          (B) TYPE: nucleic acid
234          (C) STRANDEDNESS: single
235          (D) TOPOLOGY: linear
237      (ii) MOLECULE TYPE: cDNA
239      (iii) HYPOTHETICAL: YES
241      (iv) ANTI-SENSE: NO
246      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
248 ATGGACTTAG CATTCG      16
250 (2) INFORMATION FOR SEQ ID NO: 4:
252      (i) SEQUENCE CHARACTERISTICS:
253          (A) LENGTH: 12 base pairs

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254      (B) TYPE: nucleic acid
255      (C) STRANDEDNESS: single
256      (D) TOPOLOGY: linear
258      (ii) MOLECULE TYPE: cDNA
260      (iii) HYPOTHETICAL: YES
262      (iv) ANTI-SENSE: NO
267      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
269 ATGGACTTAG CA                                     12
271 (2) INFORMATION FOR SEQ ID NO: 5:
273      (i) SEQUENCE CHARACTERISTICS:
274          (A) LENGTH: 12 base pairs
275          (B) TYPE: nucleic acid
276          (C) STRANDEDNESS: single
277          (D) TOPOLOGY: linear
279      (ii) MOLECULE TYPE: cDNA
281      (iii) HYPOTHETICAL: YES
283      (iv) ANTI-SENSE: NO
288      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
290 TGGACTTAGC AT                                     12
292 (2) INFORMATION FOR SEQ ID NO: 6:
294      (i) SEQUENCE CHARACTERISTICS:
295          (A) LENGTH: 12 base pairs
296          (B) TYPE: nucleic acid
297          (C) STRANDEDNESS: single
298          (D) TOPOLOGY: linear
300      (ii) MOLECULE TYPE: cDNA
302      (iii) HYPOTHETICAL: YES
304      (iv) ANTI-SENSE: NO
309      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
311 GGACTTAGCA TT                                     12
313 (2) INFORMATION FOR SEQ ID NO: 7:
315      (i) SEQUENCE CHARACTERISTICS:
316          (A) LENGTH: 12 base pairs
317          (B) TYPE: nucleic acid
318          (C) STRANDEDNESS: single
319          (D) TOPOLOGY: linear
321      (ii) MOLECULE TYPE: cDNA
323      (iii) HYPOTHETICAL: YES
325      (iv) ANTI-SENSE: NO
330      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
332 GACTTAGCAT TC                                     12
334 (2) INFORMATION FOR SEQ ID NO: 8:
336      (i) SEQUENCE CHARACTERISTICS:
337          (A) LENGTH: 12 base pairs
338          (B) TYPE: nucleic acid
339          (C) STRANDEDNESS: single
340          (D) TOPOLOGY: linear
342      (ii) MOLECULE TYPE: cDNA
344      (iii) HYPOTHETICAL: YES

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VERIFICATION SUMMARY

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L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]